

0420

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/748,451

DATE: 01/16/2001
TIME: 11:52:45

Input Set : A:\UTSD546USD1.txt
Output Set: N:\CRF3\01162001\I748451.raw

3 <110> APPLICANT: WANG, XIAODONG
 4 LIU, XUESONG
 6 <120> TITLE OF INVENTION: DNA FRAGMENTATION FACTOR INVOLVED IN APOPTOSIS
 8 <130> FILE REFERENCE: UTSD:546USD1
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/748,451
 11 <141> CURRENT FILING DATE: 2000-12-22
 13 <150> PRIOR APPLICATION NUMBER: 09/061,702
 14 <151> PRIOR FILING DATE: 1998-04-16
 16 <160> NUMBER OF SEQ ID NOS: 21
 18 <170> SOFTWARE: PatentIn Ver. 2.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 2839
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Homo sapiens
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 28 ggacatctgc aatgtctccag aagcccaaga gctgtaaagct gcggggccctg cgcagccg 180
 29 ggaagttcgg cgtggctggc cggagctgcc aggagggtgtc ggcgaaggcg tgcgtcccg 240
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 31 aagattactt ccccaactt cccgacaacg cccgacttgcgt gctgtccacc ttggggcagg 360
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 33 tggggctcat ccaggccggc cagcagctgc tgcgtatgtc gcaggcccc cagaggcaga 480
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 36 gatacagctg tgagagccgg atccggagtt acctgaggga ggtgagctcc taccctcca 660
 37 cagtgggtgc ggaggctcag gaaggaaattcc tgcgggtcct cggctccatg tgccagaggc 720
 38 tccggccat gcaatcataat ggcagctact tgcacagagg agccaaaggcg ggcagccg 780
 39 tctgcacacc ggaaggctgg ttctcctgcc agggccctt tgacatggc agctgcttat 840
 40 caagacactc catcaacccc tacagtaaca gggagagcag gatccttc acgacccgtga 900
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 42 aggaacaaya tggaaagagaa gtggactggg agtattttt tggcctgtt tttacctcag 1020
 43 agaacctaaa actagtgcac attgtctgcc ataagaaaaac caccacaaag ctcaactgt 1080
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 45 gccagtgaca cgtacacacc acgtctggc ctttgttga ggcctgacgt gggcatcatt 1200
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 57 atggcaaatg ggcagctcca tcctttgtt cttctaaatg cccaaaagag gtgtcatgt 1920

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See p. 5

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92      50          55          60
94 Asp Asn Ala Glu Leu Val Leu Leu Thr Leu Gly Gln Ala Trp Gln Gly
95      65          70          75          80
97 Tyr .Val Ser Asp Ile Arg Arg Phe Leu Ser Ala Phe His Glu Pro Gln
98      85          90          95
100 Val Gly Leu Ile Gln Ala Ala Gln Gln Leu Leu Cys Asp Glu Gln Ala
101      100         105         110
103 Pro Gln Arg Gln Arg Leu Leu Ala Asp Leu Leu His Asn Val Ser Gln
104      115         120         125
106 Asn Ile Ala Ala Glu Thr Arg Ala Glu Asp Pro Pro Trp Phe Glu Gly
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112 Glu Ser Arg Ile Arg Ser Tyr Leu Arg Glu Val Ser Ser Tyr Pro Ser
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116      180         185         190
118 Met Cys Gln Arg Leu Arg Ser Met Gln Tyr Asn Gly Ser Tyr Phe Asp
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122      210         215         220

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124 Ser Cys Gln Gly Pro Phe Asp Met Asp Ser Cys Leu Ser Arg His Ser
 125 225 230 235 240
 127 Ile Asn Pro Tyr Ser Asn Arg Glu Ser Arg Ile Leu Phe Ser Thr Trp
 128 245 250 255
 130 Asn Leu Asp His Ile Ile Glu Lys Lys Arg Thr Ile Ile Pro Thr Leu
 131 260 265 270
 133 Val Glu Ala Ile Lys Glu Gln Asp Gly Arg Glu Val Asp Trp Glu Tyr
 134 275 280 285
 136 Phe Tyr Gly Leu Leu Phe Thr Ser Glu Asn Leu Lys Leu Val His Ile
 137 290 295 300
 139 Val Cys His Lys Lys Thr Thr His Lys Leu Asn Cys Asp Pro Ser Arg
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 150 <211> LENGTH: 1689
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 162 163 Met Glu
 165 gtg acc ggg gac gcc ggg gta cca gaa tct ggc gag atc cgg act cta 166
 166 Val Thr Gly Asp Ala Gly Val Pro Glu Ser Gly Glu Ile Arg Thr Leu
 167 5 10 15
 169 aag ccg tgt ctg ctg cgc aac tac agc cgc gaa cag cac ggc gtg 214
 170 Lys Pro Cys Leu Leu Arg Arg Asn Tyr Ser Arg Glu Gln His Gly Val
 171 20 25 30
 173 gcc gcc tcc tgc ctc gaa gac ctg agg agc aag gcc tgt gac att ctg 262
 174 Ala Ala Ser Cys Leu Glu Asp Leu Arg Ser Lys Ala Cys Asp Ile Leu
 175 35 40 45 50
 177 gcc att gat aag tcc ctg aca cca gtc acc ctt gtc ctg gca gag gat 310
 178 Ala Ile Asp Lys Ser Leu Thr Pro Val Thr Leu Val Leu Ala Glu Asp
 179 55 60 65
 181 ggc acc ata gtg gat gat gac gat tac ttt ctg tgt cta cct tcc aat 358
 182 Gly Thr Ile Val Asp Asp Asp Tyr Phe Leu Cys Leu Pro Ser Asn
 183 70 75 80
 185 act aag ttt gtg gca ttg gct agt aat gag aaa tgg gca tac aac aat 406
 186 Thr Lys Phe Val Ala Leu Ala Ser Asn Glu Lys Trp Ala Tyr Asn Asn
 187 85 90 95
 189 tca gat gga ggt aca gct tgg att tcc caa gag tcc ttt gat gta gat 454
 190 Ser Asp Gly Gly Thr Ala Trp Ile Ser Gln Glu Ser Phe Asp Val Asp
 191 100 105 110
 193 gaa aca gac agc ggg gca ggg ttg aag tgg aat gtg gcc agg gag 502

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198	Leu	Lys	Glu	Asp	Leu	Ser	Ser	Ile	Ile	Leu	Leu	Ser	Glu	Glu	Asp	Leu	
199								135			140					145	
201	cag	atg	ctt	gtt	gac	gct	ccc	tgc	tca	gac	ctg	gct	cag	gaa	cta	cgt	598
202	Gln	Met	Leu	Val	Asp	Ala	Pro	Cys	Ser	Asp	Leu	Ala	Gln	Glu	Leu	Arg	
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205	cag	agt	tgt	gcc	acc	gtc	cag	cgg	ctg	cag	cac	aca	ctc	caa	cag	gtg	646
206	Gln	Ser	Cys	Ala	Thr	Val	Gln	Arg	Leu	Gln	His	Thr	Leu	Gln	Gln	Val	
207								165			170					175	
209	ctt	gac	caa	aga	gag	gaa	gtg	cgt	ctt	aag	cag	ctc	ctg	cag	ctg		694
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217	gag	tcc	aaa	gct	gcc	ttt	ggt	gag	gag	gtg	gat	gca	gta	gac	acg	ggt	790
218	Glu	Ser	Lys	Ala	Ala	Phe	Gly	Glu	Glu	Val	Asp	Ala	Val	Asp	Thr	Gly	
219		215						220			225						
221	atg	agc	aga	gag	acc	tcc	tgc	gac	gtt	gcg	ctg	gcg	agc	cac	atc	ctt	838
222	Met	Ser	Arg	Glu	Thr	Ser	Ser	Asp	Val	Ala	Leu	Ala	Ser	His	Ile	Leu	
223		230						235			240						
225	act	gca	ctg	agg	gag	aag	cag	gct	cca	gag	ctg	agc	tta	tct	agt	cag	886
226	Thr	Ala	Leu	Arg	Glu	Lys	Gln	Ala	Pro	Glu	Leu	Ser	Leu	Ser	Ser	Gln	
227		245						250			255						
229	gat	ttt	gag	ttt	acc	aag	gaa	gac	ccc	aaa	gca	ctg	gct	gtt	gcc		934
230	Asp	Leu	Glu	Leu	Val	Thr	Lys	Glu	Asp	Pro	Lys	Ala	Leu	Ala	Val	Ala	
231		260						265			270						
233	ttt	aac	tgg	gac	ata	aag	aag	acg	gag	act	gtt	cag	gag	gcc	tgt	gag	982
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235		275						280			285					290	
237	cgg	gag	ctc	gcc	ctg	cgc	ctg	cag	cag	acg	cag	acg	ttt	cat	tct	ctc	1030
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239		295						300			305						
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243		310						315			320						
245	cct	aag	cga	gcc	aga	cag	gat	ccc	aca	'tagcagcagc	ggaaagtgt						1125
246	Pro	Lys	Arg	Ala	Arg	Gln	Asp	Pro	Thr								
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253	aacatacgcc	gttccaccaa	ttttttttt	agccccacca	gcttcaggac	ttctgc当地											1305
255	tttgaatgt	atactgtgcac	caacaatata	ccgccttc	taattacata	tgtatgttctc											1365
257	tgttcaaaag	taattggcag	tgattggcca	ggcgcagtg	ctcacgc当地	taatccc当地											1425
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 271 <211> LENGTH: 331
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 283 35 40 45
 285 Ile Leu Ala Ile Asp Lys Ser Leu Thr Pro Val Thr Leu Val Leu Ala
 286 50 55 60
 288 Glu Asp Gly Thr Ile Val Asp Asp Asp Tyr Phe Leu Cys Leu Pro
 289 65 70 75 80
 291 Ser Asn Thr Lys Phe Val Ala Leu Ala Ser Asn Glu Lys Trp Ala Tyr
 292 85 90 95
 294 Asn Asn Ser Asp Gly Gly Thr Ala Trp Ile Ser Gln Glu Ser Phe Asp
 295 100 105 110
 297 Val Asp Glu Thr Asp Ser Gly Ala Gly Leu Lys Trp Lys Asn Val Ala
 298 115 120 125
 300 Arg Glu Leu Lys Glu Asp Leu Ser Ser Ile Ile Leu Leu Ser Glu Glu
 301 130 135 140
 303 Asp Leu Gln Met Leu Val Asp Ala Pro Cys Ser Asp Leu Ala Gln Glu
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 306 Leu Arg Gln Ser Cys Ala Thr Val Gln Arg Leu Gln His Thr Leu Gln
 307 165 170 175
 309 Gln Val Leu Asp Gln Arg Glu Glu Val Arg Gln Ser Lys Gln Leu Leu
 310 180 185 190
 312 Gln Leu Tyr Leu Gln Ala Leu Glu Lys Glu Gly Ser Leu Leu Ser Lys
 313 195 200 205
 315 Gln Glu Glu Ser Lys Ala Ala Phe Gly Glu Glu Val Asp Ala Val Asp
 316 210 215 220
 318 Thr Gly Met Ser Arg Glu Thr Ser Ser Asp Val Ala Leu Ala Ser His
 319 225 230 235 240
 321 Ile Leu Thr Ala Leu Arg Glu Lys Gln Ala Pro Glu Leu Ser Leu Ser
 322 245 250 255
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 325 260 265 270
 327 Val Ala Leu Asn Trp Asp Ile Lys Lys Thr Glu Thr Val Gln Glu Ala
 328 275 280 285
 330 Cys Glu Arg Glu Leu Ala Leu Arg Leu Gln Gln Thr Gln Ser Leu His
 331 290 295 300
 333 Ser Leu Arg Ser Ile Ser Ala Ser Lys Ala Ser Pro Pro Gly Asp Leu
 334 305 310 315 320
 336 Gln Asn Pro Lys Arg Ala Arg Gln Asp Pro Thr
 337 325 330

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
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L:371 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:412 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:445 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8